WEST Search History

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DATE: Saturday, October 28, 2006

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	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ		
☐	L7	express$3 same L2	1
☐	L6	express$5 same L2	1
☐	L3	T7 same L2	12
☐	L2	(RNA adj polymerase) same L1	43
☐	L1	(polynucleotide adj phosphorylase)	289

END OF SEARCH HISTORY

STN SEARCH #10/540,145 10/28/2006

=> index bioscience medicine

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:31:51 ON 28 OCT 2006

71 FILES IN THE FILE LIST IN STNINDEX

=> S ((polynucleotide (w)Phosphorylase)or PNPase)
22 FILE AGRICOLA
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3 FILE AQUASCI
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518 FILE BIOSIS
66 FILE BIOTECHABS
66 FILE BIOTECHDS
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16 FILE DDFU
159 FILE DGENE
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66 FILE DRUGB
21 FILE DRUGU
5 FILE EMBAL
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186 FILE ESBIOBASE
30 FILES SEARCHED...
2 FILE FROSTI
7 FILE FSTA
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28 FILE IFIPAT
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253 FILE LIFESCI
637 FILE MEDLINE
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164 FILE PASCAL
15 FILE PHAR
492 FILE SCISEARCH
143 FILE TOXCENTER
209 FILE USPATFULL
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1 FILE VETU
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60 FILE WPINDEX
68 FILES SEARCHED...
1 FILE NLDB

39 FILES HAVE ONE OR MORE ANSWERS, 71 FILES SEARCHED IN STNINDEX

L1 QUE ((POLYNUCLEOTIDE (W) PHOSPHORYLASE) OR PNPASE)

=> d rank
F1 1276 CAPLUS
F2 637 MEDLINE
F3 518 BIOSIS
F4 492 SCISEARCH
F5 362 EMBASE
F6 253 LIFESCI
F7 214 GENBANK
F8 209 USPATFULL
F9 186 ESBIOBASE
F10 170 BIOTECHNO

F11 164 PASCAL
F12 159 DGENE
F13 143 TOXCENTER
F14 66 BIOTECHABS
F15 66 BIOTECHDS
F16 66 DDFB
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F18 60 WPIDS
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F20 49 DISSABS
F21 31 BIOENG
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F31 9 CEABA-VTB
F32 7 FSTA
F33 5 ANABSTR
F34 5 EMBAL
F35 5 NTIS
F36 3 AQUASCI
F37 2 FROSTI
F38 1 VETU
F39 1 NLDB

=> file f1-f6, f8-f11, f13

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=> S L1
L2 4410 L1

=> S express? (s) L2
L3 350 EXPRESS? (S) L2

=> S purif? (s) L3
L4 19 PURIF? (S) L3

=> S (tag or his or GST or T7CBD or Trx or flag) (s) L4
L5 6 (TAG OR HIS OR GST OR T7CBD OR TRX OR FLAG) (S) L4

=> S (tag or his or GST or T7CBD or Trx or flag) (s) L3
L6 8 (TAG OR HIS OR GST OR T7CBD OR TRX OR FLAG) (S) L3

=> S (tag or his or GST or T7or CBD or Trx or flag) (s) L3
L7 8 (TAG OR HIS OR GST OR T7OR CBD OR TRX OR FLAG) (S) L3

=> s polymerase (s) L4
L8 3 POLYMERASE (S) L4

=> s polymerase (s) L7
L9 3 POLYMERASE (S) L7

=> dup rem l7
PROCESSING COMPLETED FOR L7
L10 5 DUP REM L7 (3 DUPLICATES REMOVED)

=> d ibib abs l10 1-5

L10 ANSWER 1 OF 5 USPATFULL on STN
ACCESSION NUMBER: 2006:195560 USPATFULL <<LOGINID::20061028>>
TITLE: Process for producing pnpase
INVENTOR(S): Murai, Masatoshi, Hyogo, JAPAN

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2006166315	A1	20060727
APPLICATION INFO.:	US 2003-540145	A1	20031225 (10)
	WO 2003-JP16653		20031225
			20050621 PCT 371 date

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: GREENBERG TRAURIG, LLP, MET LIFE BUILDING, 200 PARK AVENUE, NEW YORK, NY, 10166, US
NUMBER OF CLAIMS: 19
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 3 Drawing Page(s)
LINE COUNT: 695
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a process for producing ***PNPase*** , wherein ***PNPase*** can be produced easily with high efficiency, and problematic contamination with endotoxin in synthesis of a nucleic acid polymer as a raw material of pharmaceutical preparations can be reduced. ***PNPase*** is produced by Escherichia coil or the like having a T7 RNA polymerase gene, transformed with an ***expression*** vector having a ***PNPase*** gene and a T7 promoter ligated therein. For further facilitating the step of purifying ***PNPase*** , an ***expression*** vector having a ***tag*** gene is utilized and the culture time is prolonged.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2004:570017 CAPLUS <<LOGINID::20061028>>
DOCUMENT NUMBER: 141:102243
TITLE: Bacterial expression of PNPase and use in polynucleotide synthesis
INVENTOR(S): Murai, Masatoshi
PATENT ASSIGNEE(S): Nippon Shinyaku Co., Ltd., Japan

SOURCE: PCT Int. Appl., 26 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004058959	A1	20040715	WO 2003-JP16653	20031225
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2003292772	A1	20040722	AU 2003-292772	20031225
EP 1582584	A1	20051005	EP 2003-768192	20031225
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
US 2006166315	A1	20060727	US 2005-540145	20050621

PRIORITY APPLN. INFO.: JP 2002-376780 A 20021226
WO 2003-JP16653 W 20031225

AB The invention provides a process for highly efficiently and conveniently producing polynucleotide phosphorylase (PNPase) while reducing contamination with endotoxins causing problems in synthesizing a nucleic acid polymer, useful as drug synthesis starting material. PNPase is produced using Escherichia coli, etc. having a T7 RNA polymerase gene which has been transformed with an expression vector carrying a PNPase gene and a T7 promoter ligated together. Moreover, the step of purifying ***PNPase*** is simplified by using an ***expression*** vector having a ***tag*** gene or prolonging the culture time. ***Expression*** of Escherichia coli ***PNPase*** with ***His*** ***tag*** with reduced endotoxin contamination is described. Synthesis of polyinosinic acid (av. yield 50%, chain length 2200 bp) using the recombinant PNPase from inosine diphosphate trisodium salt and polycytidylic acid (av. yield 65%, chain length 2200 bp) from cytidine diphosphate trisodium salt was accomplished.

L10 ANSWER 3 OF 5 USPATFULL on STN
ACCESSION NUMBER: 2004:217827 USPATFULL <<LOGINID::20061028>>
TITLE: Cathepsin V-like polypeptides
INVENTOR(S): Tang, Y. Tom, San Jose, CA, United States
Goodrich, Ryle W., Los Angeles, CA, United States
Asundi, Vinod, Foster City, CA, United States
Drmanac, Radoje T., Palo Alto, CA, United States
PATENT ASSIGNEE(S): Nuvelo, Inc., Sunnyvale, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6783969	B1	20040831
APPLICATION INFO.:	US 2001-799451		20010305 (9)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Myers, Carla J.
NUMBER OF CLAIMS: 3
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 0 Drawing Figure(s); 0 Drawing Page(s)
LINE COUNT: 7745
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 4 OF 5 PASCAL COPYRIGHT 2006 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 1999-0215139 PASCAL <<LOGINID::20061028>>

TITLE (IN ENGLISH): ISOLATION AND CHARACTERIZATION OF THE GENE CODING FOR A PUTATIF POLYNUCLEOTIDE PHOSPHORYLASE THAT CONTAINS A BINDING DOMAIN FOR TBP (TATA-BINDING PROTEIN)

TITLE (IN FRENCH): ISOLEMENT ET CARACTERISATION D'UN GENE D'ARABIDOPSIS CODANT POUR UNE POLYNUCLEOTIDE PHOSPHORYLASE PUTATIVE INTERAGISSANT AVEC TBP (TATA-BINDING PROTEIN)

AUTHOR: KIM Yeon-Jung; MACHE Regis (dir.)

CORPORATE SOURCE: Universite de Grenoble 1, Saint-Martin-d'Heres, France (tutelle)

SOURCE: (1998-10), 150 refs.
136 p.
Dissertation Information: Universite de Grenoble 1. Saint-Martin-d'Heres. FRA, Th. doct., 98GRE10171

DOCUMENT TYPE: Dissertation

BIBLIOGRAPHIC LEVEL: Monographic

COUNTRY: France

LANGUAGE: French

SUMMARY LANGUAGE: French; English

AVAILABILITY: INIST-T 123317, T98GRE10171 0000; RBCCN-384212103, T98GRE10171 0000

AN 1999-0215139 PASCAL <<LOGINID::20061028>>

ABFR L'ARN polymerase II, l'enzyme core responsable de la synthese des ARNm chez les eucaryotes, exige des facteurs supplementaires pour l'initiation de la transcription (facteurs generaux de transcription : TFIIA, TFIID, TFIIF, TFIIE, TFIIH et TFIIJ). L'assemblage du complexe d'initiation de la transcription au niveau des elements promoteurs debute par le recrutement du facteur TFIID, qui est un facteur d'initiation essentiel constitue de la proteine de liaison a la boite TATA (TBP) et de plusieurs facteurs associees a TBP. Ces derniers sont appeles TAFs et certains semblent agir egalement comme coactivateurs qui modulent la regulation transcriptionnelle en interagissant avec divers activateurs ou represseurs transcriptionnels. Le but de ce travail consistait a rechercher des proteines qui interagiraient avec la proteine TBP2 d'Arabidopsis. Les connaissances actuelles concernant la composition du complexe d'initiation de la transcription par l'ARN polymerase II etaient limitees aux systemes humains, de Drosophiles ou de levures. Peu d'information etait disponible concernant le systeme vegetal a l'exception de certaines proteines TBP isolees chez quelques especes. Nous avions utilise le systeme double hybride de la levure pour cribler une banque d'ADNc d'A. thaliana et un clone positif a ete finalement isole. L'ADNc ainsi isole a ete introduit dans un vecteur d' ***expression*** d'E. coli pour une surproduction de la proteine sous forme de fusion a la ***GST*** . L'analyse de l'interaction proteine-proteine in vitro en utilisant la proteine (TIP : TBP Interacting Polypeptide) surexprimee et la proteine cible TBP fusionnee a un enchainement d'histidine a confirme l'interaction directe entre TIP et TBP. Une experience de gel retard a prouve que TIP empeche TBP2 de se lier a la boite TATA in vitro. Afin de trouver le gene et l'ADNc complet, une banque genomique et une deuxieme banque d'ADNc ont ete criblees avec le fragment d'ADNc precedemment isole comme sonde. Un fragment d'ADN d'approximativement 7 kb contenant le gene entier, et un ADNc, codant une proteine d'environ 110 kDa, ont ete obtenus et sequences. La comparaison de sequence utilisant le logiciel BLAST a revele une forte homologie avec la ***PNPase*** d'E. coli (***polynucleotide*** ***phosphorylase***) au niveau du domaine N-terminal de la proteine. Mais le domaine C-terminal contenant l'activite de liaison a TBP ne montre aucune similitude particuliere avec d'autres proteines. Nous avons montre, par co-immunoprecipitation, que cette proteine complete interagit avec TBP in vitro. En outre, le resultat d'une analyse de RNase protection indique que le gene est transcrit constitutivement en un ARNm presentant un intron non episse (retention d'intron). Cet ARNm incompletement episse semble coder pour la proteine tronquee, ce qui est du a la presence de codons stop dans l'intron. L'epissage de cet intron semble etre regule de facon tissu-specifique et par des stress

environnementaux : c'est a dire que l'ARNm completement episse est trouve seulement dans les graines et les siliques et dans les plantes traitees au froid. Base sur l'ensemble des resultats, l'implication de la proteine ainsi identifiee dans la regulation de l' ***expression*** des genes est discutee.

L10 ANSWER 5 OF 5 LIFESCI COPYRIGHT 2006 CSA on STN DUPLICATE 2
ACCESSION NUMBER: 96:73885 LIFESCI <<LOGINID::20061028>>
TITLE: Proteins associated with RNase E in a multicomponent ribonucleolytic complex
AUTHOR: Miczak, A.; Kaberdin, V.R.; Wei, Chia-Li; Lin-Chao, Sue*
CORPORATE SOURCE: Inst. Mol. Biol., Academia Sinica, Nankang Taipei, Taiwan 11529
SOURCE: PROC. NATL. ACAD. SCI. USA, (1996) vol. 93, no. 9, pp. 3865-3869.
ISSN: 0027-8424.
DOCUMENT TYPE: Journal
FILE SEGMENT: N; J
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The Escherichia coli endoribonuclease RNase E is essential for RNA processing and degradation. Earlier work provided evidence that RNase E exists intracellularly as part of a multicomponent complex and that one of the components of this complex is a 3'-to-5' exoribonuclease, ***polynucleotide*** ***phosphorylase*** (EC 2.7.7.8). To isolate and identify other components of the RNase E complex, ***FLAG*** -epitope-tagged RNase E (***FLAG*** -Rne) fusion protein was purified on a monoclonal antibody-conjugated agarose column. The ***FLAG*** -Rne fusion protein, eluted by competition with the synthetic ***FLAG*** peptide, was found to be associated with other proteins. N-terminal sequencing of these proteins revealed the presence in the RNase E complex not only of ***polynucleotide*** ***phosphorylase*** but also of DnaK, RNA helicase, and enolase (EC 4.2.1.11). Another protein associated only with epitope-tagged temperature-sensitive (Rne-3071) mutant RNase E but not with the wild-type enzyme is GroEL. The ***FLAG*** -Rne complex has RNase E activity in vivo and in vitro. The relative amount of proteins associated with wild-type and Rne-3071 ***expressed*** at an elevated temperature differed.

=> d his

L1 QUE ((POLYNUCLEOTIDE (W) PHOSPHORYLASE) OR PNPASE)

FILE 'CAPLUS, MEDLINE, BIOSIS, SCISEARCH, EMBASE, LIFESCI, USPATFULL, ESBIOBASE, BIOTECHNO, PASCAL, TOXCENTER' ENTERED AT 17:34:20 ON 28 OCT 2006
L2 4410 S L1
L3 350 S EXPRESS? (S) L2
L4 19 S PURIF? (S) L3
L5 6 S (TAG OR HIS OR GST OR T7CBD OR TRX OR FLAG) (S) L4
L6 8 S (TAG OR HIS OR GST OR T7CBD OR TRX OR FLAG) (S) L3
L7 8 S (TAG OR HIS OR GST OR T7OR CBD OR TRX OR FLAG) (S) L3
L8 3 S POLYMERASE (S) L4
L9 3 S POLYMERASE (S) L7
L10 5 DUP REM L7 (3 DUPLICATES REMOVED)

=> log y

NiceZyme View of ENZYME: EC 2.7.7.8

Official Name

Polyribonucleotide nucleotidyltransferase.

Alternative Name(s)

Polynucleotide phosphorylase.

Reaction catalysed

RNA(n+1) + phosphate <=> RNA(n) + a nucleoside diphosphate

Comment(s)

ADP, IDP, GDP, UDP and CDP can act as donors.

Cross-references

Biochemical Pathways; map number(s)	H1 ; H2 ; J7 ; K7 ; J8 ; K8
BRENDA	2.7.7.8
PUMA2	2.7.7.8
PRIAM enzyme-specific profiles	2.7.7.8
KEGG Ligand Database for Enzyme Nomenclature	2.7.7.8
IUBMB Enzyme Nomenclature	2.7.7.8
IntEnz	2.7.7.8
MEDLINE	Find literature relating to 2.7.7.8
MetaCyc	2.7.7.8
UniProtKB/Swiss-Prot	Q8TCS8, PNPT1_HUMAN; Q8K1R3, PNPT1_MOUSE; Q5RCW2, PNPT1_PONPY; P50849, PNP_BACSU; P57454, PNP_BUCAI; Q8K9H5, PNP_BUCAP; Q89AF8, PNP_BUCBP; P05055, PNP_ECOLI; P44584, PNP_HAEIN; P41121, PNP_PHOLU; O87792, PNP_PSEPU; Q9ZD43, PNP_RICPR; O34275, PNP_YEREN;

View entry in original ENZYME format
View entry in raw text format (no links)

All UniProtKB/Swiss-Prot entries referenced in this entry, with possibility to download in

KEGG ENZYME: 2.7.7.8

Help

Entry	EC 2.7.7.8 Enzyme
Name	polyribonucleotide nucleotidyltransferase; polynucleotide phosphorylase; PNPase; nucleoside diphosphate:polynucleotidyl transferase; polyribonucleotide phosphorylase
Class	Transferases Transferring phosphorus-containing groups Nucleotidyltransferases
Sysname	polyribonucleotide:phosphate nucleotidyltransferase
Reaction (IUBMB)	RNA(n+1) + phosphate = RNA(n) + a nucleoside diphosphate [RN:R07282]
Reaction (KEGG)	R07282 > R00437 R00438 R00439 R00440 Show all
Substrate	RNAn+1 [CPD:C00046]; phosphate [CPD:C00009]
Product	RNAn [CPD:C00046]; nucleoside diphosphate [CPD:C00454]
Comment	ADP, IDP, GDP, UDP and CDP can act as donors.
Pathway	PATH: map00230 Purine metabolism PATH: map00240 Pyrimidine metabolism
Ortholog	KO: K00962 polyribonucleotide nucleotidyltransferase
Genes	HSA: 87178(PNPT1) PTR: 459247 MMU: 71701(Pnpt1) RNO: 360992(Pnpt1) CFA: 481376(LOC481376) GGA: 421206(PNPT1) DME: Dmel_CG11337 CEL: BE0003N10.1 ATH: At5g14580(T15N1.70) CME: CMH146C CMQ324C CAL: orf19.1578(RRP5) ECO: b3164(pnp) ECE: Z4525(pnp) ECS: ECs4045 ECC: c3920(pnp) ECI: UTI89_C3594(pnp) ECP: ECP_3252 STY: STY3463(pnp) STT: t3200(pnp) SPT: SPA3149(pnp) SEC: SC3223(pnp) STM: STM3282(pnp) YPE: YPO3490(pnp)